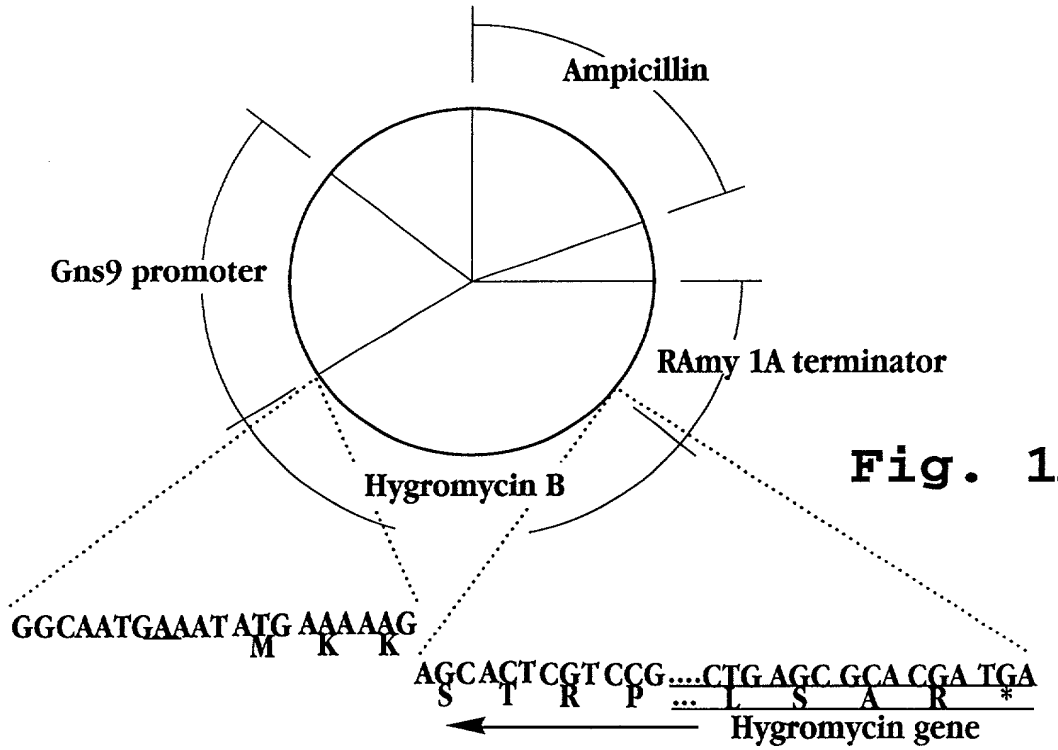


Fig. 1A

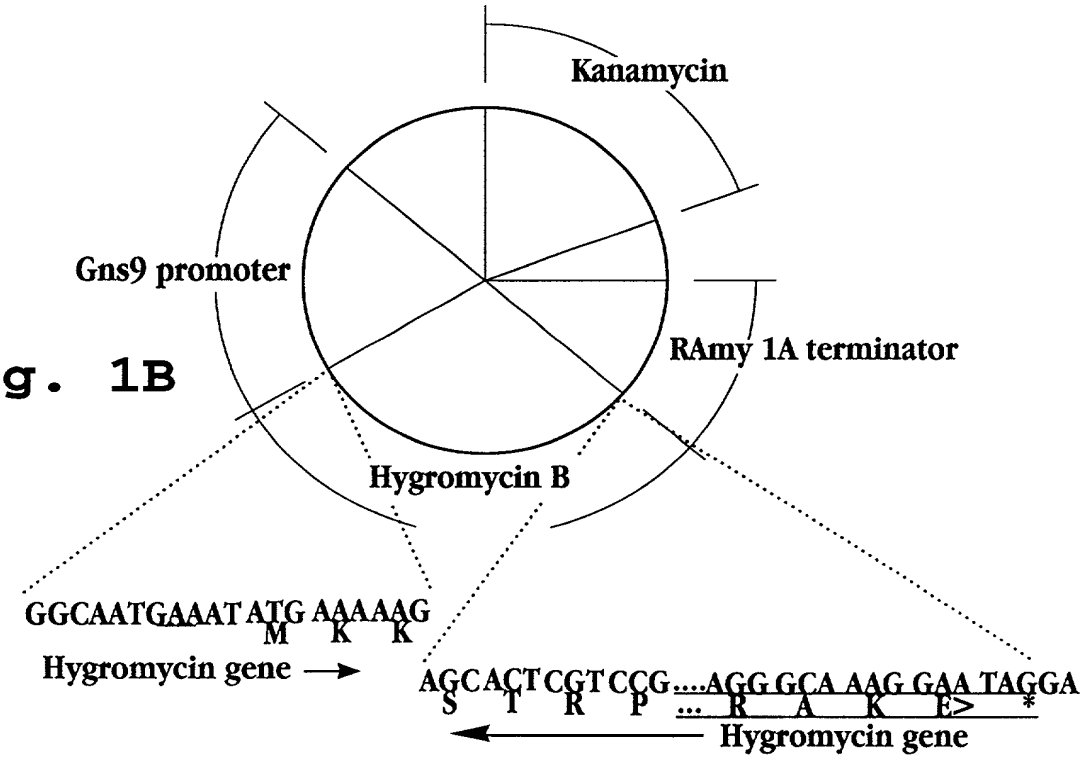


Fig. 1B

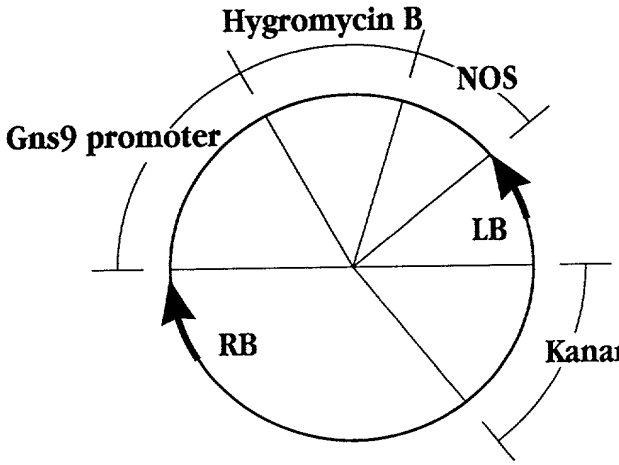


Fig. 1C

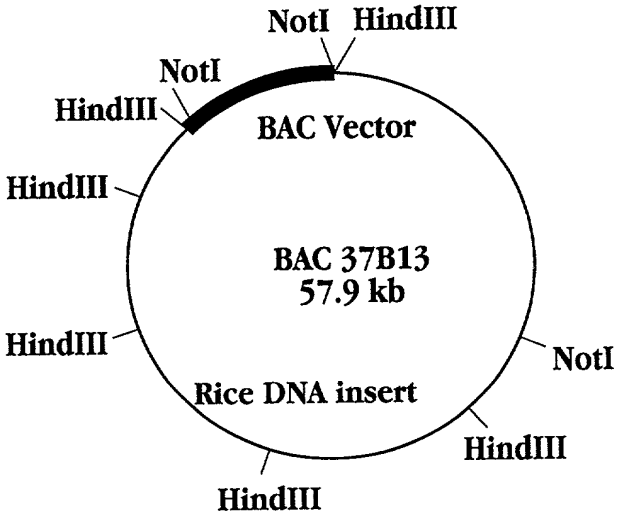


Fig. 3A

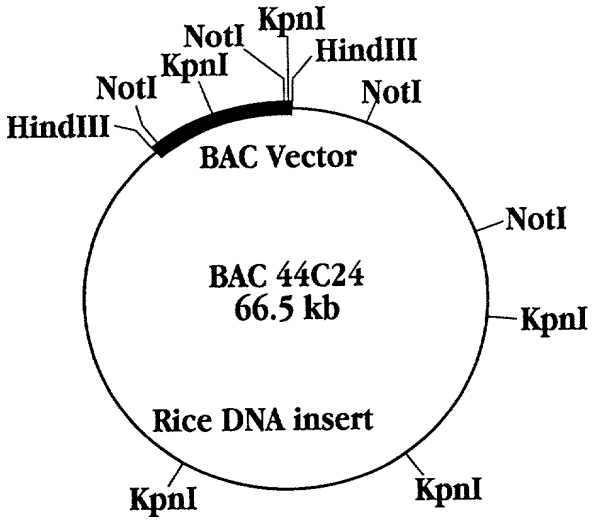
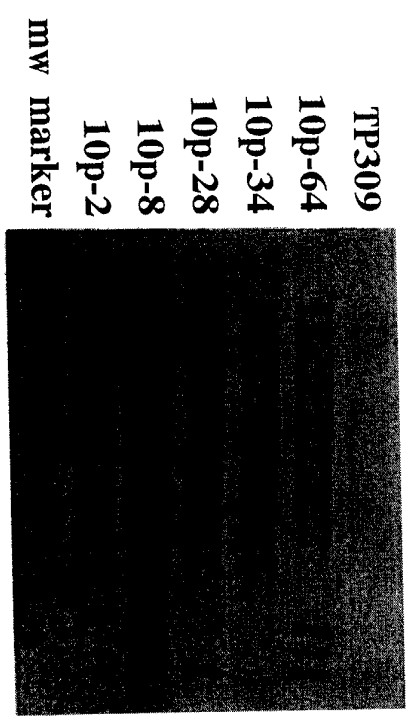
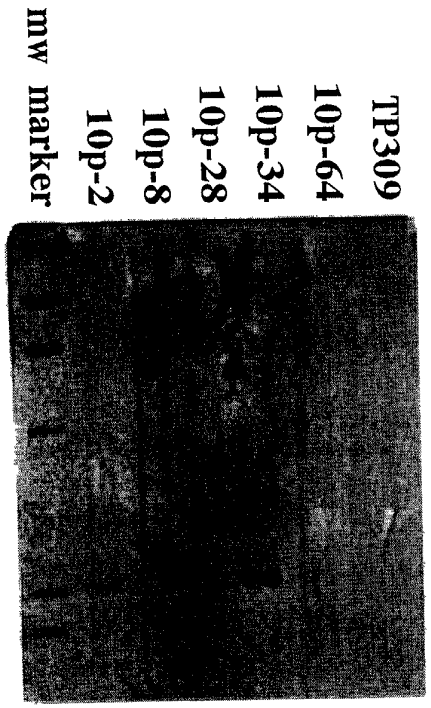


Fig. 3B



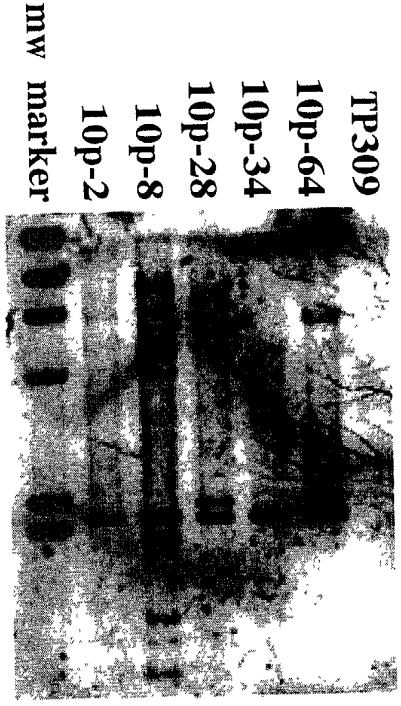
pAPI25

Fig. 2A



pAPI65

Fig. 2B



pAPI96

Fig. 2C

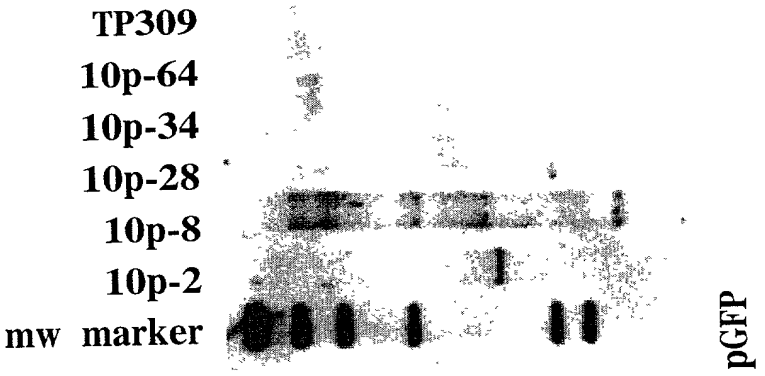


Fig. 2F

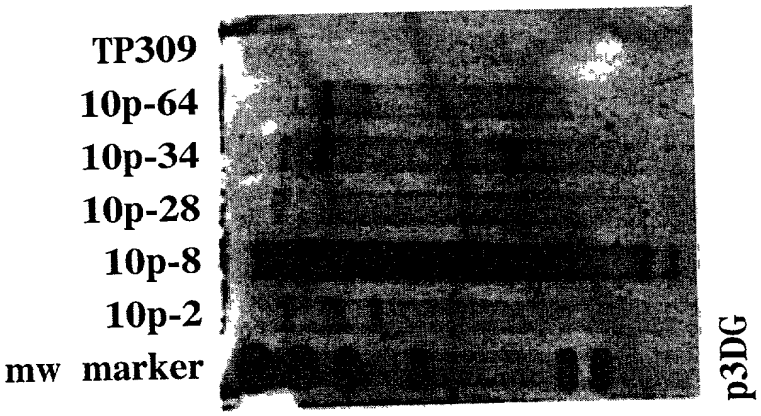


Fig. 2E

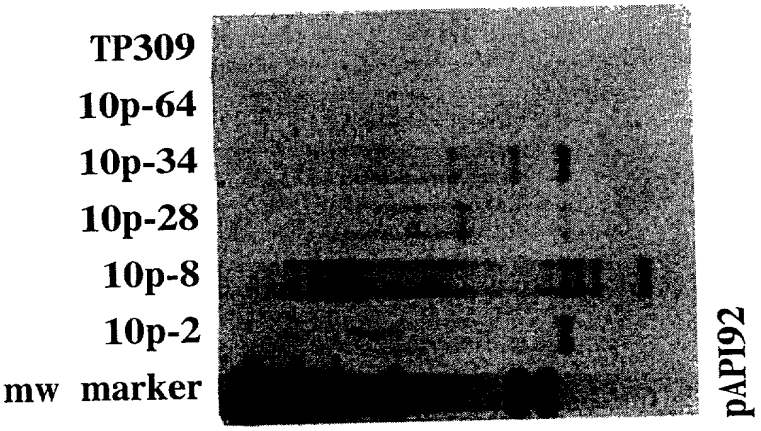
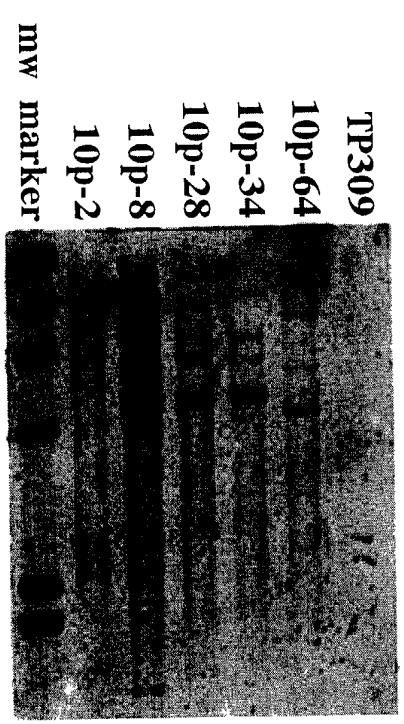
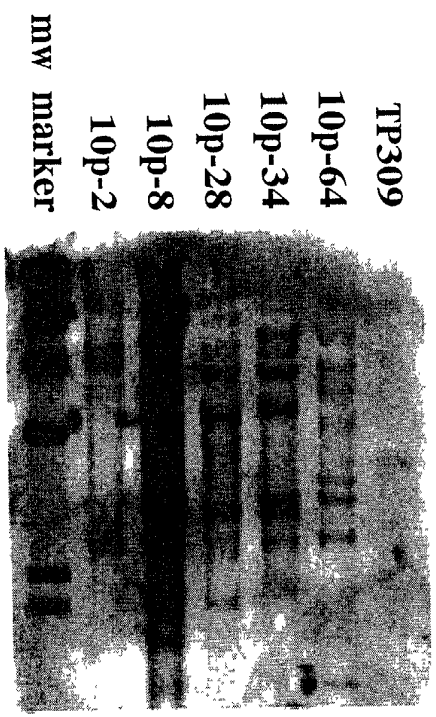


Fig. 2D



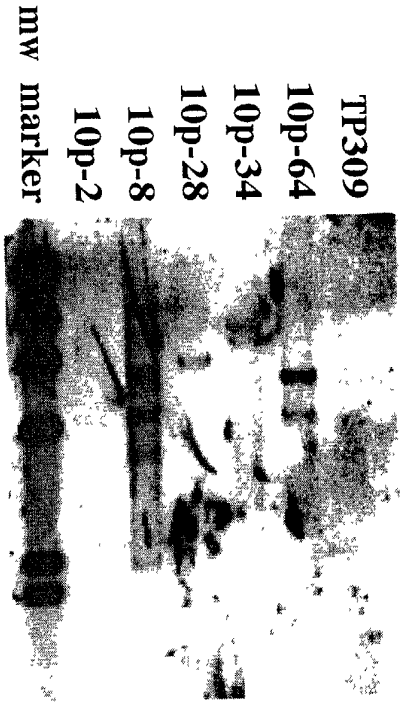
pAPI76

Fig. 2G



pAHC20

Fig. 2H

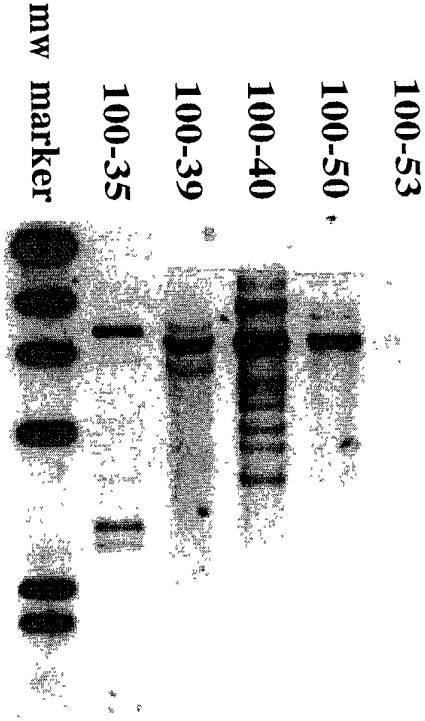


pAH18

Fig. 2I

37B13

Fig. 4A



44C24

Fig. 4B

```
       10        20        30        40        50        60        70
CACCTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTT
GTGGATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAA

       80        90       100       110       120       130       140
AACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTG
TTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAAC

      150       160       170       180       190       200       210
TTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTA
AAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGAT

      220       230       240       250       260       270       280
TCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCA
AGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGT

      290       300       310       320       330       340       350
CTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAA
GATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTT

      360       370       380       390       400       410       420
AGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAAC
TCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTG

      430       440       450       460       470       480       490
CACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCCCATTCGCCATTCAGGCTGCGCAACTGT
GTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGGGTAAGCGGTAAGTCCGACGCGTTGACA

      500       510       520       530       540       550       560
TGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC
ACCCTTCCCGCTAGCCACGCCCGGAGAAGCGATAATGCGGTCGACCGCTTTCCCCCTACACGACGTTCCG

      570       580       590       600       610       620       630
GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATA
CTAATTCAACCCATTGCGGTCCCAAAAGGGTCAGTGCTGCAACATTTTGCTGCCGGTCACTTAACATTAT

          >_Gns9_Promoter
     |
      640       650       660       670       680       690       700
CGACTCACTATAGGGCGAATTGGAGCTCAACTTTAGTCCATATATTTAGACACTAATTTAGAGTATTAAA
GCTGAGTGATATCCCGCTTAACCTCGAGTTGAAATCAGGTATATAAATCTGTGATTAAATCTCATAATTT

      710       720       730       740       750       760       770
TATAAATTACTTACAAAACTAATTCAATAAATGAAAGCTAATTTGCGAGACAAATTTTTATGTTTAATT
ATATTTAATGAATGTTTTGATTAAGTTATTTACTTTCGATTAAACGCTCTGTTTAAAAATACAAATTAA
```

FIG. 5A

```
      780       790       800       810       820       830       840
AATCCATAATTAGAGAATGTTTACTGTAGCATCACATAGACTAATCATGGATTAATTAGGCTCAATAGAT
TTAGGTATTAATCTCTTACAAATGACATCGTAGTGTATCTGATTAGTACCTAATTAATCCGAGTTATCTA

      850       860       870       880       890       900       910
TCGTCTCGTGAATTAGTCCAAGATTATGGATGGATTTTATTAATAGTCTACGTTTAATATTTATAATTAG
AGCAGAGCACTTAATCAGGTTCTAATACCTACCTAAAATAATTATCAGATGCAAATTATAAATATTAATC

      920       930       940       950       960       970       980
TGTTCAAACATCCGATGTGATAGGGACTTAAAAAGTTTAGTCCCATCTAAACAGGGCCACAGTCTATGTG
ACAAGTTTGTAGGCTACACTATCCCTGAATTTTTCAAATCAGGGTAGATTTGTCCCGGTGTCAGATACAC

      990      1000      1010      1020      1030      1040      1050
GAGCATGTTCACCGAACACCGATAAATATTGCAAAGCCCAGAATGATTTTGGTCCCACATGCCAGAAACT
CTCGTACAAGTGGCTTGTGGCTATTTATAACGTTTCGGGTCTTACTAAAACCAGGGTGTACGGTCTTTGA

     1060      1070      1080      1090      1100      1110      1120
ACCACACCCACATTTCGGTTCATTTTCAGCTCAGGAAAATCGTCCAACAATTTCAGCTCAGGAAATTAAA
TGGTGTGGGTGTAAAGCCAAGTAAAAGTCGAGTCCTTTTAGCAGGTTGTTAAAGTCGAGTCCTTTAATTT

     1130      1140      1150      1160      1170      1180      1190
TCGTCCGAGAAAGGAACAAGTTTGGAGCCGTTGGGATGAGAGCAATTAGGTCACGCTTAACTACAAGTAC
AGCAGGCTCTTTCCTTGTTCAAACCTCGGCAACCCTACTCTCGTTAATCCAGTGCGAATTGATGTTCATG

     1200      1210      1220      1230      1240      1250      1260
AGTCTCATTCATCGACATTGATTAGCCAGCAACTAACCACTTAACCCCGAGCCAGCCCAAGCGCTCCGTA
TCAGAGTAAGTAGCTGTAACTAATCGGTCGTTGATTGGTGAATTGGGGCTCGGTCGGGTTCGCGAGGCAT

     1270      1280      1290      1300      1310      1320      1330
CGTTCGTTGGGCCCCCGCCGCGCAGGCGGAGACAACGGTCATCCGGCGCGCCGGTCGCTCTCCCTCGCTC
GCAAGCAACCCGGGGGCGGCGCGTCCGCCTCTGTTGCCAGTAGGCCGCGCGGCCAGCGAGAGGGAGCGAG

     1340      1350      1360      1370      1380      1390      1400
GCACGGCCGCACCACCCACTTCGCCACGAACCCGACGCGAGCGCGACGTGCATCTCCCAACATCCCCGCC
CGTGCCGGCGTGGTGGGTGAAGCGGTGCTTGGGCTGCGCTCGCGCTGCACGTAGAGGGTTGTAGGGGCGG

     1410      1420      1430      1440      1450      1460      1470
ATTTCCTCCCCACCCAAAACCAACCCGCCCGCGTGCGGCTGGCCCACTTTACAGCGCCTCACCTCCCCCA
TAAAGGAGGGGTGGGTTTTGGTTGGGCGGGCGCACGCCGACCGGGTGAAATGTCGCGGAGTGGAGGGGGT

     1480      1490      1500      1510      1520      1530      1540
ACCATAAATCCCCGCCCTTTTCCCCCCCCTCTCCACCACTCACCACGCTCTCCACTACACGACTCGTCGCC
TGGTATTTAGGGGCGGGAAAAGGGGGGGAGAGGTGGTGAGTGGTGCGAGAGGTGATGTGCTGAGCAGCGG

     1550      1560      1570      1580      1590      1600      1610
GTCTTGCTCTGCTGCCTCTCGCGCCCGCGCAGCAGTGAGCAGCAGCAAGAGCAGTCTAGGGGGATCTACC
CAGAACGAGACGACGGAGAGCGCGGGCGCGTCGTCACTCGTCGTCGTTCTCGTCAGATCCCCCTAGATGG
```

FIG. 5B

```
          1620        1630        1640        1650        1660
ATG AGC CCA GAA CGA CGC CCG GCC GAC ATC CGC CGT GCC ACC GAG GCG GAC ATG
TAC TCG GGT CTT GCT GCG GGC CGG CTG TAG GCG GCA CGG TGG CTC CGC CTG TAC
 M   S   P   E   R   R   P   A   D   I   R   R   A   T   E   A   D   M>
___a___a___a___a___a___a___a___BAR GENE____a___a___a___a___a___a___a___>

    1670        1680        1690        1700        1710
CCG GCG GTC TGC ACC ATC GTC AAC CAC TAC ATC GAG ACA AGC ACG GTC AAC TTC
GGC CGC CAG ACG TGG TAG CAG TTG GTG ATG TAG CTC TGT TCG TGC CAG TTG AAG
 P   A   V   C   T   I   V   N   H   Y   I   E   T   S   T   V   N   F>
___a___a___a___a___a___a___a___BAR GENE____a___a___a___a___a___a___a___>

          1720        1730        1740        1750        1760
1770
CGT ACC GAG CCG CAG GAA CCG CAG GAG TGG ACG GAC GAC CTC GTC CGT CTG CGG
GCA TGG CTC GGC GTC CTT GGC GTC CTC ACC TGC CTG CTG GAG CAG GCA GAC GCC
 R   T   E   P   Q   E   P   Q   E   W   T   D   D   L   V   R   L   R>
___a___a___a___a___a___a___a___BAR GENE____a___a___a___a___a___a___a___>

    1780        1790        1800        1810        1820
GAG CGC TAT CCC TGG CTC GTC GCC GAG GTG GAC GGC GAG GTC GCC GGC ATC GCC
CTC GCG ATA GGG ACC GAG CAG CGG CTC CAC CTG CCG CTC CAG CGG CCG TAG CGG
 E   R   Y   P   W   L   V   A   E   V   D   G   E   V   A   G   I   A>
___a___a___a___a___a___a___a___BAR GENE____a___a___a___a___a___a___a___>

 1830        1840        1850        1860        1870        1880
TAC GCG GGC CCC TGG AAG GCA CGC AAC GCC TAC GAC TGG ACG GCC GAG TCG ACC
ATG CGC CCG GGG ACC TTC CGT GCG TTG CGG ATG CTG ACC TGC CGG CTC AGC TGG
 Y   A   G   P   W   K   A   R   N   A   Y   D   W   T   A   E   S   T>
___a___a___a___a___a___a___a___BAR GENE____a___a___a___a___a___a___a___>

          1890        1900        1910        1920        1930
GTG TAC GTC TCC CCC CGC CAC CAG CGG ACG GGA CTG GGC TCC ACG CTC TAC ACC
CAC ATG CAG AGG GGG GCG GTG GTC GCC TGC CCT GAC CCG AGG TGC GAG ATG TGG
 V   Y   V   S   P   R   H   Q   R   T   G   L   G   S   T   L   Y   T>
___a___a___a___a___a___a___a___BAR GENE____a___a___a___a___a___a___a___>

    1940        1950        1960        1970        1980
CAC CTG CTG AAG TCC CTG GAG GCA CAG GGC TTC AAG AGC GTG GTC GCT GTC ATC
GTG GAC GAC TTC AGG GAC CTC CGT GTC CCG AAG TTC TCG CAC CAG CGA CAG TAG
 H   L   L   K   S   L   E   A   Q   G   F   K   S   V   V   A   V   I>
___a___a___a___a___a___a___a___BAR GENE____a___a___a___a___a___a___a___>

          1990        2000        2010        2020        2030
2040
GGG CTG CCC AAC GAC CCG AGC GTG CGC ATG CAC GAG GCG CTC GGA TAT GCC CCC
CCC GAC GGG TTG CTG GGC TCG CAC GCG TAC GTG CTC CGC GAG CCT ATA CGG GGG
 G   L   P   N   D   P   S   V   R   M   H   E   A   L   G   Y   A   P>
___a___a___a___a___a___a___a___BAR GENE____a___a___a___a___a___a___a___>
```

FIG. 5C

```
    2050        2060        2070        2080        2090
CGC GGC ATG CTG CGG GCG GCC GGC TTC AAG CAC GGG AAC TGG CAT GAC GTG GGT
GCG CCG TAC GAC GCC CGC CGG CCG AAG TTC GTG CCC TTG ACC GTA CTG CAC CCA
 R   G   M   L   R   A   A   G   F   K   H   G   N   W   H   D   V   G>
___a___a___a___a___a___a___a___BAR GENE____a___a___a___a___a___a___a___>

2100        2110        2120        2130        2140        2150
TTC TGG CAG CTG GAC TTC AGC CTG CCG GTA CCG CCC CGT CCG GTC CTG CCC GTC
AAG ACC GTC GAC CTG AAG TCG GAC GGC CAT GGC GGG GCA GGC CAG GAC GGG CAG
 F   W   Q   L   D   F   S   L   P   V   P   P   R   P   V   L   P   V>
___a___a___a___a___a___a___a___BAR GENE____a___a___a___a___a___a___a___>

        2160      2170
ACC GAG ATC TGA TGACCCTC
TGG CTC TAG ACT ACTGGGAG
 T   E   I   *>
___BAR GENE____>

        >NOS_Terminator

    2180      2190      2200      2210      2220      2230      2240
GAGTCTAGACGCGTCCCGAATTTCCCCGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATC
CTCAGATCTGCGCAGGGCTTAAAGGGGCTAGCAAGTTTGTAAACCGTTATTTCAAAGAATTCTAACTTAG

    2250      2260      2270      2280      2290      2300      2310
CTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACAT
GACAACGGCCAGAACGCTACTAATAGTATATTAAAGACAACTTAATGCAATTCGTACATTATTAATTGTA

    2320      2330      2340      2350      2360      2370      2380
GTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCG
CATTACGTACTGCAATAAATACTCTACCCAAAAATACTAATCTCAGGGCGTTAATATGTAAATTATGCGC

    2390      2400      2410      2420      2430      2440      2450
ATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGATC
TATCTTTTGTTTTATATCGCGCGTTTGATCCTATTTAATAGCGCGCGCCACAGTAGATACAATGATCTAG

    2460      2470      2480      2490      2500      2510      2520
GGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCGGTACCCAGCTTTTGTTCCC
CCCTTAAGCTATAGTTCGAATAGCTATGGCAGCTGGAGCTCCCCCCCGGGCCATGGGTCGAAAACAAGGG

    2530      2540      2550      2560      2570      2580      2590
TTTAGTGAGGGTTAATTTCGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCC
AAATCACTCCCAATTAAAGCTCGAACCGCATTAGTACCAGTATCGACAAAGGACACACTTTAACAATAGG

    2600      2610      2620      2630      2640      2650      2660
GCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGC
CGAGTGTTAAGGTGTGTTGTATGCTCGGCCTTCGTATTTCACATTTCGGACCCCACGGATTACTCACTCG
```

FIG. 5D

```
     2670      2680      2690      2700      2710      2720      2730
TAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATT
ATTGAGTGTAATTAACGCAACGCGAGTGACGGGCGAAAGGTCAGCCCTTTGGACAGCACGGTCGACGTAA

     2740      2750      2760      2770      2780      2790      2800
AATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGA
TTACTTAGCCGGTTGCGCGCCCCTCTCCGCCAAACGCATAACCCGCGAGAAGGCGAAGGAGCGAGTGACT

     2810      2820      2830      2840      2850      2860      2870
CTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCC
GAGCGACGCGAGCCAGCAAGCCGACGCCGCTCGCCATAGTCGAGTGAGTTTCCGCCATTATGCCAATAGG

     2880      2890      2900      2910      2920      2930      2940
ACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAA
TGTCTTAGTCCCCTATTGCGTCCTTTCTTGTACACTCGTTTTCCGGTCGTTTTCCGGTCCTTGGCATTTT

     2950      2960      2970      2980      2990      3000      3010
AGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAG
TCCGGCGCAACGACCGCAAAAAGGTATCCGAGGCGGGGGGACTGCTCGTAGTGTTTTTAGCTGCGAGTTC

     3020      3030      3040      3050      3060      3070      3080
TCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGC
AGTCTCCACCGCTTTGGGCTGTCCTGATATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAGCACGCG

     3090      3100      3110      3120      3130      3140      3150
TCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTT
AGAGGACAAGGCTGGGACGGCGAATGGCCTATGGACAGGCGGAAAGAGGGAAGCCCTTCGCACCGCGAAA

     3160      3170      3180      3190      3200      3210      3220
CTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGA
GAGTATCGAGTGCGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTCGACCCGACACACGTGCT

     3230      3240      3250      3260      3270      3280      3290
ACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACAC
TGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGGCCATTGATAGCAGAACTCAGGTTGGGCCATTCTGTG

     3300      3310      3320      3330      3340      3350      3360
GACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAG
CTGAATAGCGGTGACCGTCGTCGGTGACCATTGTCCTAATCGTCTCGCTCCATACATCCGCCACGATGTC

     3370      3380      3390      3400      3410      3420      3430
AGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAA
TCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTCCTGTCATAAACCATAGACGCGAGACGACTT

     3440      3450      3460      3470      3480      3490      3500
GCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGT
CGGTCAATGGAAGCCTTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTTTGGTGGCGACCATCGCCACCA
```

FIG. 5E

```
      3510      3520      3530      3540      3550      3560      3570
TTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTA
AAAAAACAAACGTTCGTCGTCTAATGCGCGTCTTTTTTTCCTAGAGTTCTTCTAGGAAACTAGAAAAGAT

      3580      3590      3600      3610      3620      3630      3640
CGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGAT
GCCCCAGACTGCGAGTCACCTTGCTTTTGAGTGCAATTCCCTAAAACCAGTACTCTAATAGTTTTTCCTA

      3650      3660      3670      3680      3690      3700      3710
CTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGG
GAAGTGGATCTAGGAAAATTTAATTTTTACTTCAAAATTTAGTTAGATTTCATATATACTCATTTGAACC

      3720      3730      3740      3750      3760      3770      3780
TCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAG
AGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATC

      3790      3800      3810      3820      3830      3840      3850
TTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAAT
AACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCCGAATGGTAGACCGGGGTCACGACGTTA

      3860      3870      3880      3890      3900      3910      3920
GATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAG
CTATGGCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTTGGTCGGTCGGCCTTCCCGGCTC

      3930      3940      3950      3960      3970      3980      3990
CGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAA
GCGTCTTCACCAGGACGTTGAAATAGGCGGAGGTAGGTCAGATAATTAACAACGGCCCTTCGATCTCATT

      4000      4010      4020      4030      4040      4050      4060
GTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTC
CATCAAGCGGTCAATTATCAAACGCGTTGCAACAACGGTAACGATGTCCGTAGCACCACAGTGCGAGCAG

      4070      4080      4090      4100      4110      4120      4130
GTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGC
CAAACCATACCGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGGGTACAACACG

      4140      4150      4160      4170      4180      4190      4200
AAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCA
TTTTTTCGCCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAACCGGCGTCACAATAGTGAGT

      4210      4220      4230      4240      4250      4260      4270
TGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGA
ACCAATACCGTCGTGACGTATTAAGAGAATGACAGTACGGTAGGCATTCTACGAAAAGACACTGACCACT

      4280      4290      4300      4310      4320      4330      4340
GTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGG
CATGAGTTGGTTCAGTAAGACTCTTATCACATACGCCGCTGGCTCAACGAGAACGGGCCGCAGTTATGCC
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FIG. 5F

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     4350      4360      4370      4380      4390      4400      4410
GATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAAC
CTATTATGGCGCGGTGTATCGTCTTGAAATTTTCACGAGTAGTAACCTTTTGCAAGAAGCCCCGCTTTTG

     4420      4430      4440      4450      4460      4470      4480
TCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGC
AGAGTTCCTAGAATGGCGACAACTCTAGGTCAAGCTACATTGGGTGAGCACGTGGGTTGACTAGAAGTCG

     4490      4500      4510      4520      4530      4540      4550
ATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATA
TAGAAAATGAAAGTGGTCGCAAAGACCCACTCGTTTTTGTCCTTCCGTTTTACGGCGTTTTTTCCCTTAT

     4560      4570      4580      4590      4600      4610      4620
AGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTT
TCCCGCTGTGCCTTTACAACTTATGAGTATGAGAAGGAAAAAGTTATAATAACTTCGTAAATAGTCCCAA

     4630      4640      4650      4660      4670      4680      4690
ATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATT
TAACAGAGTACTCGCCTATGTATAAACTTACATAAATCTTTTTATTTGTTTATCCCCAAGGCGCGTGTAA

      4700
TCCCCGAAAAGTGC
AGGGGCTTTTCACG
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FIG. 5G